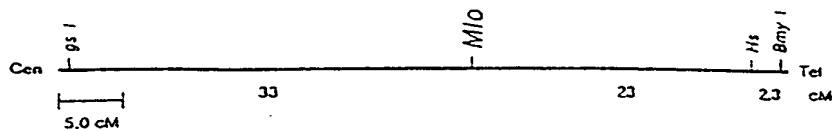


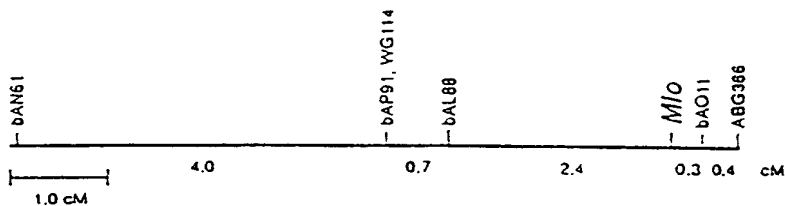
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Morphological
marker map



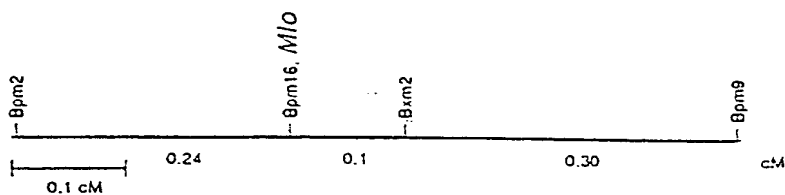
RFLP map

(CarlsbergII *Mlo* x
Grannenlose Zweizeilige *mlo-11*)

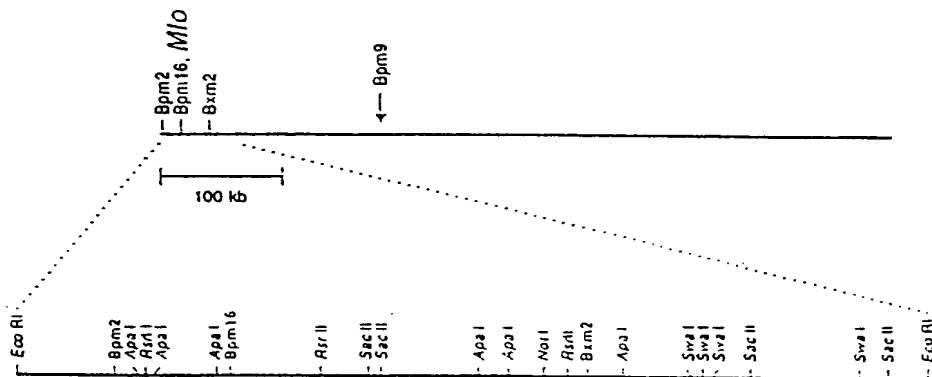


AFLP map

(Ingrid *Mlo* x BC Ingrid *mlo-3*)

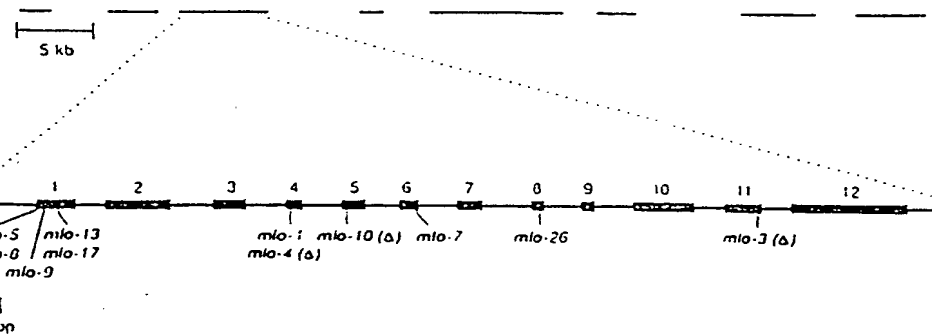


YAC YHV303-A6



BAC F15

Sequence contigs



Mlo gene structure

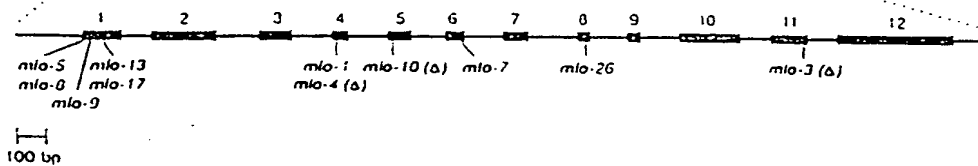


Figure 1

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M S D K K G V P A R E L P E T P S W A V
 ATGTCGGACAAAAAGGGGTGCCGGCGCGGGAGCTGCCGGAGACGCCGTCGTGGCGGGT 60
 A V V F A A M V L V S V L M E H G L H K
 GCGGTGGTCTTCGCCGCCATGGTGCTCGTGTCCGTCTCATGGAACACGGCCTCCACAAG 120
 L G H W F Q H R H K K A L W E A L E K M
 CTCGGCCATTGGTTCCAGCACCGGCACAAGAAGGCCCTGTGGGAGGCGCTGGAGAAGATG 180
 K A E L M L V G F I S L L L I V T Q D P
 AAGGCGGAGCTCATGCTGGTGGGCTTCATATCCCTGCTCCTCATCGTCACGCAGGACCCC 240
 I I A K I C I S E D A A D V M W P C K R
 ATCATGCCAAGATATGCATCTCCGAGGATGCCGCCGACGTCATGTGGCCCTGCAAGCGC 300
 G T E G R K P S K Y V D Y C P E G K V A
 GGCACCGAGGGCCGAAGCCCAGCAAGTACGTTGACTACTGCCCGGAGGGCAAGGTGGCG 360
 L M S T G S L H Q L H V F I F V L A V F
 CTCATGTCCACGGGCAGCTTGACCAGCTGCACGTCTTCATCTTCTGCTCGCGGTCTTC 420
 H V T Y S V I T I A L S R L K M R T W K
 CATGTACCTACAGCGTCATCACCATAGCTCTAAGCCGTCTCAAAATGAGAACATGGAAG 480
 K W E T E T T S L E Y Q F A N D P A R F
 AAATGGGAGACAGAGACCACCTCCTTGGAAATACCAGTTCGCAAATGATCCTGCACGGTTC 540
 R F T H Q T S F V K R H L G L S S T P G
 CGGTTACAGCACAGACGTCGTTCTGTAAGCGCCACCTGGGCCTCTCCAGCACCCCTGGC 600
 I R W V V A F F R Q F F R S V T K V D Y
 ATCAGATGGGTGGTGGCCTTCTTCAGGCAGTTCCTCAGGTCAGTCACCAAGGTGGACTAC 660
 L T L R A G F I N A H L S Q N S K F D F
 CTGACCTTGAGGGCAGGCTTCATCAACGCGCATTGTGCGAAAACAGCAAGTTCGACTTC 720
 H K Y I K R S M E D D F K V V V G I S L
 CACAAGTACATCAAGAGGTGCGATGGAGGACGACTTCAAGGTGCTGCTCGGCATCAGCCTC 780
 P L W G V A I L T L F L D I N G V G T L
 CCGCTGTGGGGTGTGGCGATCCTCACCTCTTCTTGACATCAATGGGGTTGGCAGCTC 840
 I W I S F I P L V I L L C V G T K L E M
 ATCTGGATTCTTTCATCCCTCTCGTGATCTCTTGTGTGTTGGAACCAAGCTGGAGATG 900
 I I M E M A L E I Q D R A S V I K G A P
 ATCATCATGGAGATGGCCCTGGAGATCCAGGACCGGGCGAGCGTCATCAAGGGGGCCCCC 960
 V V E P S N K F F W F H R P D W V L F F
 GTGGTTCGAGCCCAGCAACAAGTTCTTCTGGTTCCACCGCCCCGACTGGGTCTCTTCTTC 1020
 I H L T L F Q N A F Q M A H F V W T V A
 ATACACCTGACGTTGTTCCAGAACCGGTTTCAGATGGCGCATTTTGTGTGGACAGTGGCC 1080
 T P G L K K C Y H T Q I G L S I M K V V
 ACCCCCCGCTTGAAGAAATGCTACCACACGCAGATCGGGCTGAGCATCATGAAGGTGGTG 1140
 V G L A L Q F L C S Y M T F P L Y A L V
 GTGGGGCTAGCTCTCCAGTTCCTCTGCAGCTATATGACCTTCCCCCTCTACGCGCTCGTC 1200
 T Q M G S N M K R S I F D E Q T S K A L
 ACACAGATGGGATCAACATGAAGAGGTCCATCTTCGACGAGCAGACGTCCAAGCGGCTC 1260
 T N W R N T A K E K K K V R O T D M L M
 ACCAAGTGGCGGAACACGGCCAAGGAGAAGAAGAAAGTCCGAGACACGGACATGCTGATG 1320
 A Q M I G D A T P S R G S S P M P S R G
 GCTCAGATGATCGCGACGCAACACCGAGCCGAGGCTCGTCGCCGATGCCGAGCCGGGGC 1380

Figure 2

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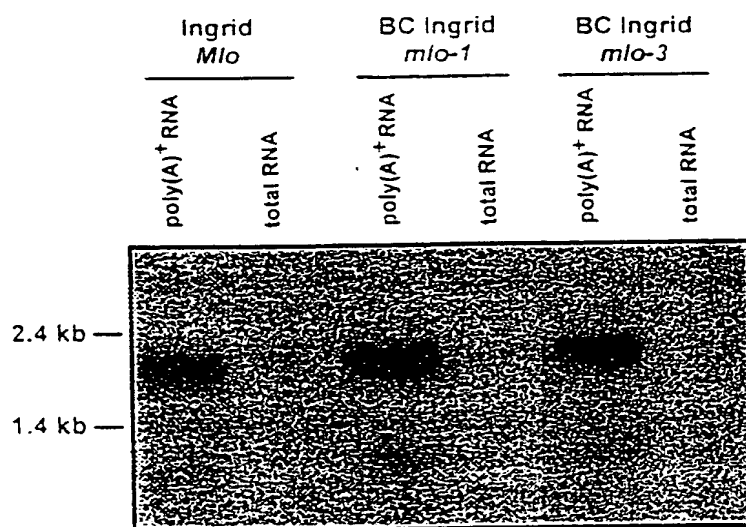
Figure 2 (Continued)

S S P V H L L H K G M G R S D D P Q S A 1440
TCATCACCCGTGCACCTGCTTCACAAGGGCATGGGGCGGTGCGACGACCCCCAGAGCGCG
P T S P R T Q Q E A R D M Y P V V V A H 1500
CCCACCTCGCCAAGGACCCAGCAGGAGGCTAGGGACATGTACCCGGTGTGGTGGCGCAC
P V H R L N P N D R R R S A S S S A L E 1560
CCGGTGACAGACTAAATCCTAACGACAGGAGGAGGTCCGCCTCGTCGTCGGCCCTCGAA
A D I P S A D F S F S Q G *
GCCGACATCCCCAGTGCAGATTTTTCCTTCAGCCAGGGATGA 1602

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Figure 3



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Figure 4

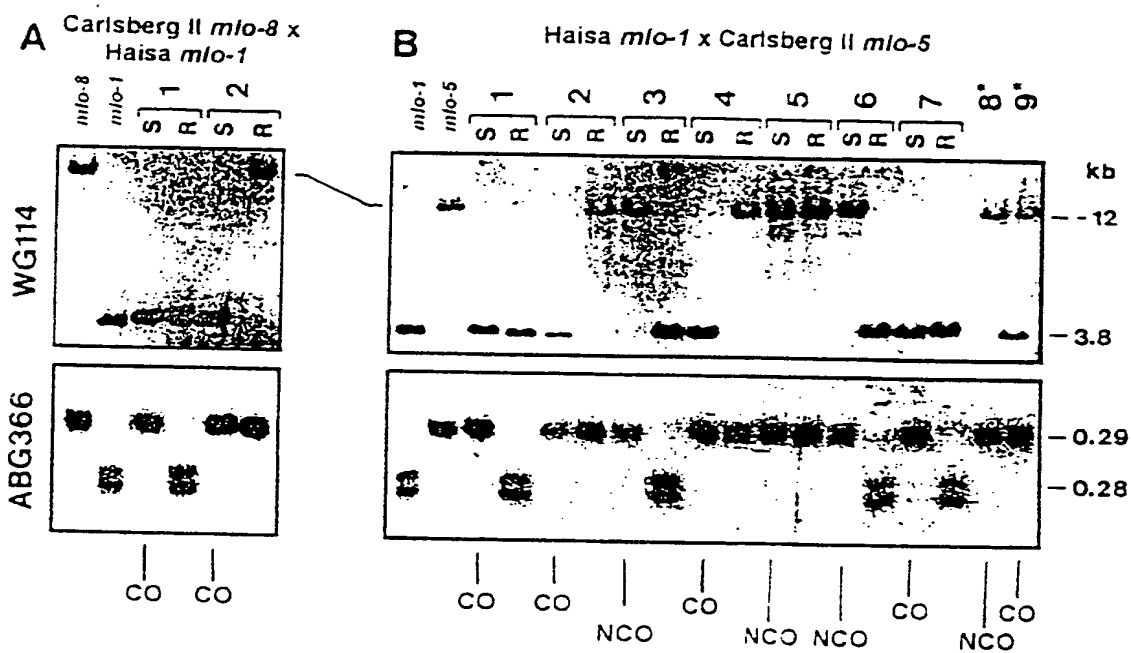


FIGURE 5

SUBSTITUTE SHEET (RULE 26)

FIGURE 5 c nt'd

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1047 AAGCGCCACCTGGG...CCTCTCCAGCACCCCTGGCATCAGATGGGTGGT 1093
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 836 AAGCGGCATCTGGGATCATTCTCAAGCACCCCTGGGCTCAGATGGATCGT 885
 1094 GAGTTTTTTTAGCTTCTTATCTGCCCCCTCATCTGTGTGTAATGTT..... 1137
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 886 GAGTTATCAATCTCCGAAT.....ACATGCTTGTTTTTTATTCTTGCA 928
 1138 ..TGGCGTA.....TGGAGTCAGGTGATTT.....ACCTT 1165
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 929 ACTGGCCTAGCTGTTCCAATTCAATCCATATTTTTTGAAAAAAAAAATAT 978
 1166 GCCTGTGATGTTTGTGTCCTTGTGAGGTGGCCTTCTTCAGGCAGTTCTTC 1215
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 979 TCATGCCGTGTTTG.....TTGTTAGGTAGCATTCTTCAGGCAGTTCTTT 1023
 1216 AGGTCAGTCACCAAGGTGGACTACCTGACCTTGAGGGCAGGCTTCATCAA 1265
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1024 GGGTCCGTCACCAAGGTGGACTACCTGACCATGCGGCAAGGCTTCATCAA 1073
 1266 CGTACGTGC...CTCCCCCTTAGCTCCGCCATTGCTGCCGCGATGTAG 1311
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1074 TGTATATACTAATCAAACCTGACCAATTCAACATTGATGATGC.AAACAG 1122
 1312 CAGCAAAGCTTCT.....CAAGTTATCCTTCTGACGCTAAAGTTCCCA 1354
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1123 AAGACCAGGTTTTTTTTTTCCGAGTTGTGCAT.TGAAGTTAATG..... 1165
 1355 TGTTTTTTCTCAAATTATTCTGCGCAGGCG.CATTTGTCGCAAAACAGC 1403
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1166 .GTTTTAGCTTC...TTCTCTTTTGAGGCGCCATTGTGCGCAGAATAGC 1211
 1404 AAGTTCGACTTCCACAAGTACATCAAGAGGTGATGGAGGACGACTTCAA 1453
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1212 AAGTTCGACTTCCACAATAACATCAAGAGGTCTTTGGAGGACGACTTCAA 1261
 1454 GGTGCTCGTCCGTCATCAGGTACGTTCCATTCTCTCTGACCAGACCA 1503
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1262 AGTTGTGCTTGGCATCAGGTCCG.....TCCTCGCTTT..... 1294
 1504 CACCCCATGGATAGATTTTAAACAATTGCTGTCAGGTCCACATGATAACA 1553
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1295ATTAATTATAGGA....CTCTTATATTCAACATTTTTTTT 1330
 1554 ATATACTATGA.ACTTGGTCTTTGCTCCTTGTCTTG.....CACGATCA 1597
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1331 ATAAAGAAACATATTTAGTCT...CCAGTTGTGTATGTGTATGTGGATCT 1377
 1598 TGACACATTGGCCTGTTTTTCGAGCCTCCGCTGTGGGGTGTGGCGATC 1647
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1378 TGACACATTGG.CTGGTTTTGCAGCCTCCCTCTGTGGTTCGTCGGAATC 1426
 1648 CTCACCTCTCTCTTGACATCAATGGTATGGACCTTCTCCTCTCCGTTT 1697
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1427 CTTGTACTCTTCTCGATATCCACGTA..ATCCTTGTCT.....ATTT 1469
 1698 CTCTATTGCTTTGCAGCTAAATAAAACACTTGCAATTCGTCTCGTGATCA 1747
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1470 CATTCTTTTTTTTACTCTCAAAACCTTGTTCTGAATTGGTCTTATAATCA 1519
 1748 CCGCTCATTTTTCAACCATTTCTTTTTCTACTCATAGGGGTTGGCAGCT 1797
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1520 CCATCGATTTTTTTTTCAACTT.TTCCCCGCGTGTAGGTCTTGGCACACT 1568
 1798 CATCTGGATTCTTTTCATCCCTCTCGTGGTAAGTGC.AGATTTCTCC.AT 1845
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1569 TATTTGGATCTCTTTTGTCTCTCATCGTAAGAGCGAAATTTCCCTGT 1618

1846 CGAAAGCAACGACCAAACCAATT.....TGATCGCAAT 1878
| | | | | | | | | | | | | | | | | |
1619 CCAAAGAAACAGTTAACATAATTAATTATGCTTTAATTTATCATGAAAAT 1668

1879 GGAAACCCACACCTAATATTAACCTCAAATGTCAATTGTCGGTGCCTCTT 1928
| | | | | | | | | | | | | | | | | |
1669 TAATATGATCATATAACTAATGAACAAACATTCA..TGTGAATGCCACCG 1716

1929 CCTCAACAGATCCTCTTGTGTGTTGGAACCAAGCTGGAGATGATCATCAT 1978
| | | | | | | | | | | | | | | | | |
1717 TTGTCTCAGATCGTCTTGTTAGTTGGGACCAAGCTAGAGATGGTGATCAT 1766

1979 GGAGATGGCCCTGGAGATCCAGGACCGGGCGAGCGTCATCAAGGGGGCCC 2028
| | | | | | | | | | | | | | | | | |
1767 GGAGATGGCCCAAGAGATACAGGACAGGGCCACTGTGATCCAGGGAGCAC 1816

2029 CCGTGGTTCGAGCCCGCAACAAGTTCTTCTGCTTCCACCGCCCCGACTCG 2078
| | | | | | | | | | | | | | | | | |
1817 CTATGGTTGAACCAAGCAACAAGTACTTCTGGTTCAACCGCCCTGACTGG 1866

2079 GTCCTCTTCTTCATACACCTGACGTTGTT..... 2107
| | | | | | | | | | | | | | | | | |
1867 GTCTTGTTCCTTCATACACCTGACACTCTCCCATGTACATGTTTTAAACC 1916

:
:

2108CCAGAACGC.GTTTCAGATGGCGCATTTTG 2136
| | | | | | | | | | | | | | | | | |
2017 GACGGACGGATCGATCATCACCAGAACGCATTTTCAGATGGCGCATTTCG 2066

2137 TGTGGACAGTG....GTACGCCAC.....CGATGAÄCTTGTCAGTT 2173
| | | | | | | | | | | | | | | | | |
2067 TATGGACTATGGTGTGTATGCTACTTGCTTAGTTGTTGCCATTATCAGTT 2116

2174AACATGGGTGTCA...AGGCACCGAGTGCCGCTGATGA..... 2208
| | | | | | | | | | | | | | | | | |
2117 CTTAAGCAAATTAAGTGTGATGCATGCACTGA.....CTAATGAGACAA 2160

2209ÄCTGCTCTGACGGAGATTTACTTGTGTTGT.....AGGCC 2243
| | | | | | | | | | | | | | | | | |
2161 AAAATGACACAGCTTGTCATCGATCTGGTTGTTTTGTGTGTGACAGGCA 2210

2244 ACGCCCGGCTTGAAGAAATGCTACCACACGCAGATCGGGCTGAGCATCAT 2293
| | | | | | | | | | | | | | | | | |
2211 ACACCTGGTCTGAAGAAATGCTTCCATGAAAATATTTGGCTGAGCATCGT 2260

2294 GAAGGTGGTGGTGGGGCTAGCTCTCCAGTTCTCTGAGCTATATGACCT 2343
| | | | | | | | | | | | | | | | | |
2261 GGAAGTCATTGTGGGGATCTCTCTTCAGGTGCTATGCAGCTACATCACCT 2310

2344 TCCCGCTCTACGCGCTCGTACACAGGTAATAAAACCGTCCAGGAA 2389
| | | | | | | | | | | | | | | | | |
2311 TCCCGCTCTACGCGCTCGTACACAGGTGAACAAGCCATTACAAA 2356

[illegible]

FIGURE 6 c nt'd

[illegible]

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FIGURE 6 cont'd

2632 CGGGGCTCATCACCGTGCACCTGCTTCACAAGGGCATGGGGCGGTCCGA 2681
 2108GTGCACCTGCTCCACAAGGCCGGGGCGCGGTCCGA 2142
 2682 CGACCCCCAGAGCGCGCCACCTCGCCCAAGGACCCAGCAGGAGGCTAGGG 2731
 2143 CGACCCCCAGAGCGTGC CGGCGTCCCCGAGGGCCGAGAAGGAAGGCGGCG 2192
 2732 ACATGTACCCGGTTGTGGTGGCGCACCCGGTGCACAGACTAAATCCTAAC 2781
 2193 GC.....GTGCAGCATCCGGCGCGCAAGGTACCTCCTTGT 2227
 2782 GACAGGAGGAGGTCCGCCTCGTCGTCGGCCCTCGAAGCCGACATCCCCAG 2831
 2228 GACGGGTGGAGGTCGGCCTCGTCGCCGCGCTCGACGCTCACATCCCCGG 2277
 2832 TGCAGATTTTTCCTTCAGC.....CAGGGATGAGACAAGTTTCTG 2871
 2278 TGCAGATTTTGGCTTCAGCACGCAACGTTGACCGATCAGACAAGTTCCTT 2327
 2872 TATT 2875
 2328 TTTT 2331

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Figure 7

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	GGCTGCTCCGCCAGCAACACAGACACAGCAGCGTACCTGCGT	
	ACGTAGCGTGCGCTTTCTTTTTCCTTTTCGCTCTCTTGCTGCTCGGCCGGCCACG	
	TGCATAGCCGCCACGGCCAGGCACCTCGCGGTTGCGTCGCGTGCATCTGCGTGTGCGTA	
	CCTGGTAGAGGCGGCCGTCTGCTTGTCTCGGGCAAGGAAGCGTTGCGGCGGTCCAGCG	
helix I	M S D K K G V P A R E L P E T P S W R O N N V	20
	ATGTCGGACAAAAAAGGGTGC CGGCGCGGAGCTGCGGAGACGCGTCGTGGCGGTG	60
	A D V V V F A A M V L V S V L M E H G L H K	40
	GCGGTGGTCTTCGCGCCATGGTGTCTGCTGCTGCTCATGGAACACGGCCTCCACAAG	120
	L G H W F Q H R H K K A L W E A L E K M	60
	CTCGGCCATTGGTTCAGACCGCGCACAGAAGGCCCTGTGGGAGGCGCTGGAGAGATG	180
helix II	K A E L M L V G F I S L L L F V S T S O U R D A A R	80
	AAGGCGGAGCTCATGCTGCTGGGCTTCATATCCCTGCTCTCATGTCACGCAGGACCC	240
	I M I S A K K I C I S E D A A D V M W P C K R	100
	ATCATCGCCAGATATGCATCTCGAGGATGCGCGCAGCTCATGTGGCCCTGCAGCGC	300
	G T E G R K P S K Y V D Y C P E G K V A	120
	GGCACCGAGGGCCGCAAGCCAGCAAGTACGTTGACTACTGCCGAGGGCAAGGTGGCG	360
helix III	L M S T G S L H Q L H V F I F V L L A R V A R F	140
	CTCATGTCCAGGGCAGCTTGACACAGCTGCAGCTCTTCATCTTCGTGCTCGCGTCTTC	420
	H V T Y S V I T I A L S R L K M R T W K	160
	CATGTACCTACAGCGTCATCACCATAGCTCTAAGCCGTCTCAAAATGAGAACATGGAG	480
	K W E T E T T S L E Y Q F A N D P A R F	180
	AAATGGGAGACAGAGACCACCTCCTTGGATACAGTTCCGAATGATCCTGCACGGTTC	540
	R F T H Q T S F V K R H L G L S S T P G	200
	CGGTCACGCACAGACGTCGTTTCGTGAAGCGCCACCTGGGCTCTCCAGCACCCCTGGC	600
	I R W V V A F F R Q F F R S V T K V D Y	220
	ATCAGATGGGTGGTGGCTTCTTCAGGCAGTTCTCAGGTCACTACCAAGGTGGACTAC	660
	L T L R A G F I N A H L S Q N S K F D F	240
	CTGACCTTGAGGGCAGGCTTCATCAACGCGCATTGTGCGAAACAGCAAGTTCGACTTC	720
helix IV	H K Y I K R S M E D D F K V V V G I I S I L	260
	CACAAGTACATCAAGAGGTCGATGGAGGACGACTCAAGGTCTGCTGGCATCGGCTC	780
helix V	P L W G V A I L T L F L D I N G V G T S L	280
	CGGCTGTGGGGTGTGGCGATCCTCACCCTCTTCCTTGACATCAATGGGTTGGCAGCTC	840
	I W I S F I P L V I L L C V G T K L E M	300
	ATCTGGATTCTTTCATCCCTCTCTGTCCTCTGTTGTGTGGAACCAAGCTGGAGATG	900
	I I M E M A L E I Q D R A S V I K G A P	320
	ATCATCATGGAGATGGCCCTGGAGATCCAGGACCGGGCGAGCTCATCAAGGGCGCC	960
	V V E P S N K F F W F H R P D W V L F F	340
	GTGGTCGAGCCAGCAACAAGTCTCTGGTTCACCGCCCGGCTGGGCTCTCTCTTC	1020
	I H L T L F Q N A F Q M A H F V W T V A	360
	ATACACCTGACGTTGTTCAGAAGCGGTTTCAGATGGCGCATTTGTGTGGACAGTGGCC	1080
helix VI	T P G L K K C Y H T Q I G L S I M K V A V	380
	ACGCCGGGCTTGAAGAAATGCTACCACACGAGATCGGGCTGAGCATCATGAAGGTGGTG	1140
	V G L A A D Q F L C S Y M T F P L Y A L A V	400
	GTGGGCTAGCTCTCCAGTTCCTCTGCGAGCTATATGACCTTCCCTCTACGCGCTCGTC	1200
	T Q M G S N M K R S I P D E Q T S K A L	420
	ACACAGATGGGATCAACATGAAGAGGTCCATCTTCGACGAGCAGCTCAAGGCGCTC	1260
	T N W R N T A K E K K K V R D T D M L M	440
	ACCAACTGGCGGAACAGCGCAAGGAGAAGAAGAAAGTCCGAGACACGGACATGCTGATG	1320
	A Q M I G D A T P S R G S S P M P S R G	460
	GCTCAGATGATCGGCGACGCAACACCGAGCGGAGCTCTGCGCGATGCGGAGCCGGGGC	1380
	S S P V H L L H K G M G R S D D P Q S A	480
	TCATACCCGTGCACCTGCTTCAAGGGCATGGGGCGGTGGGACGACCCCGAGCGCG	1440
	P T S P R T Q Q S A R D M Y P V V V A H	500
	CCCACCTCGCAAGGACCCAGCAGGAGGCTAGGACATGTACCCGGTTGTGGTGGCGCAC	1500
	P V H R L N P N D R R R S A S S S A L E	520
	CCGGTG CACAGACTAAATCCTAAGCAGAGGAGGTCGGCTCTGCTGCGGCCCTCGAA	1560
	A O I P S A D F S F S Q G	
	GCGGACATCCCAAGTGAGATTTTCTTCAGCCAGGATGAGACAAGTTCTGTATTCA	
	TGTTAGTCCCAATGTATAGCCAACATAGGATGTATGATTGCTACAATAAGAAATACAT	
	TTTTACTGAGTC	

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Figure 8

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1 GAATTCAATT AAGGACAACA ACGGATGATA GGCTTAAGCT AGAGAGGATT
 51 CATATGGATT AATTAAGTGT ACTTAAGTTG AGGTAAAAGT CTATCGATTG
 101 CTTTGGACAC CGGCTCTCCC ATGATCTGCC AAGTTGAGCC GGCCTACCTA
 151 ATTTCTTTCG AAAGCACACA ACAAACGAAG GTAACCACTA ATCTAGACAC
 201 CACGCCTAAG TTATCAATTA CTACTCTAGT CTCGCGTAGA AACTTCATTG
 251 TTTATGGAGA GTGCTAGTAC TAGAGTACTT AATATAATAG TAAGCGACAA
 301 ACCCAGCAGC ATGAGAATGT ACCTCACTTA CGTAGTCAAT TAAGTCGAAA
 351 AGGAAATCTT GAACACTTAC TTTATTAAAG AAGTATTCCC CGAGGTACAG
 401 GAGAGGAGAG CACGCCAATA ACTCCAGCAC TCCTCCGAAA CCTTCTCACC
 451 TCTCTACCCT TTTTCTCCAC ACAACTAAAA TGATGTCTAA TGTATGAAA
 501 TGAGTTGTAC TCTATTTTGT TGTGTGTTTG GAAGTGAAAT TAGCTCATCC
 551 TTTTATAGCA ACTTAATGGT CGGTTGTAGG TTGGTAATTA AGTCGGTAAA
 601 CACTCACAAC CACCATCGTC AACCAATAGG AGATCGCCAC ATGATCGAAA
 651 GCTGACAGTT AGGGGTGCCA ACCCTGTTTT GTCCGAACCA ACCAAACAAC
 701 CTCTATCTAG GACCTCTCTT CTATCTCTGA CAAGTCGGCC CATATGCGGG
 751 TGCACATATG ATTAAGTCAA TTTCAGTCGT TTTGGACTGT CATGTGGGCC
 801 CTTCCAATCC TTGTGCTCCC ATATGATTGG TCGAAAGTAC ATTTAATTCC
 851 TGGGTGAGTG CTAGAACTAA TATGATAGAT GTGCTCCGGC TCCTGGGAAA
 901 GAGGCCACTT GACATACTTG GGGTAGTGCC CCAAGGGTAT TCCCTATCGC
 951 TTTTTCATAA TTTTCTCTCT CCAAAATCGG ACGGAAACAA TAAAAAGAG
 1001 AGGCGATGTT CATCGGCAAA TATCTATTTT TTTGATAGTG TCTTCCCTTA
 1051 AAACCTTGATT TTTGCGAAGA CTTCCGGCTA AAACCATGAA ATCAGAGTTC
 1101 CTTGTAAACA ATTTAATTTG CCTAAATACA AAAAAAGATCG AATGGAGATA
 1151 GCATTAAACT TGCTCCATAC GAATCATATT AGTTGGACCG TAACTCATAG
 1201 AAAAACTTGC AAGTTGGTTG ACCTATCAAC CCTCTTATGT TGACCGTAAA
 1251 CCTGTTATGC ATTAAGGATT AAGTACCGGC AGATCGTCAC TACTCACGAA
 1301 TGCACAAATT TCCGGTAACG TAGGATGGGA TGAGTTGGTC ACAAACGGGT
 1351 CACCACGTCG CCAACCTGCG CCGGATCGAG CCATTGGCCG GCGATGCACG
 1401 CGCTTTGACA CAGCCGCCCCG CCGCCCCCGG GCGCGCCCCG GTTTTAAATA
 1451 AAAACCGGCC GCCCCCTGTC AAAGGTCTCA AAGTGTCAAG TGCATCAGAG
 1501 CTAAGCTAGC GGTCAACCCAG TCAGCTCACC CCGAGACGCA CCAGGGGATC
 1551 TATUGGATCA TGGCAGGTGG GAGATCGGGA TCGCGGGAGT TGCCGGAGAC
 1601 GCCGACGTGG GCGGTGGCCG TCGTCTGCGC CGTCCTCGTG CTCCTCTCCG
 1651 CCGCCATGGA GCACGGCCTC CACAACCTCA GCCATGTACG CCGCGCGGCA
 1701 CGCGGTGTGC TCATCTCTCG AGTTAATTTG GTTGTGTTG TTGTTGTGTT
 1751 CTTGTGACAT CTCAATTAAC ATCCGATCGT GTCGATCGA TCGCCCTGTG
 1801 GTGGCGATAC TCCTTGCATT GCAGTGCTTC CGTAGCGGGC AGAAGAGGC
 1851 CATGCGCGAC GCGCTCGACA AGATCAAGC AGGTCAACCT CAGCCTCAGC

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FIGURE 8 cont'd

1901 TCACCCTCAG CCTCCATCTC TAAATATTTG ACGCCGTTGA CTTTTTTAAA
1951 TATGTTTGAC CATTCGTCTT ATTTAAAAAA TTTAAGTAAT TATTAATTCT
2001 TTTTCTACCA TTTGATTCAT TGCTAAATAT ACTATTATGT ATACATATAG
2051 TTTTACATAT TTCACTAAAG TTTTTAAATA AGACGAATGG TCAAACATGT
2101 TTAAAAAAGT CAACGGCGTC AAACATTTAG GAAGAAGAGA ATATTATATT
2151 GCTGCTCCCC TCTAGCCACT TTGCTGCCTC CCTCGTCATT TTTTCAAGTA
2201 TTTTACGCAA GACTGGTCCT CCAAATCAAA CGTCACAAAT AAGCCATTTA
2251 TAGTTTCCTT TCGCTTTTTA AGGGGGACTA CTTGTATTTA ATCATGGAGG
2301 AAACACCAG TCGGATGTCC GATTACTTAA AAAAAAATTC GGGGGACTAA
2351 TTTTTTTGGC TGATCATCGG TGAAATATTA GGTTATATAT GTTGAAAAAA
2401 AATCAGCCAC AAACAATGAA ATATTTTGTG AAACACATAT TAGACACGTT
2451 GAAACGTATC ATTGTTACGT ATAAAACATC GAATGTTAAC AGATTAAAAC
2501 ATATGTTTTT TTTTAATCAG AATATAATCA TGCGATATAT TATTGTAAAG
2551 ATATAATTAC AACGAATACA ACAGTGCAT CGGATTATAT ATATATTAGT
2601 AGTTTAAGAG AAAAATCATT TTGAAGATTA CTAGATACAT ACACGTATAG
2651 ATGGATGAAG TGGAGAGAGA TTAGAGATAA GTAGTTATAT GAATTTTGTG
2701 AAACACACTT AAGACATATG TTCAAACATA CTGCTATTAT GTATGAAATA
2751 TTGAGTTTTA ACGGTTTAAA ACACATATTC TTTTAATTAG AATGTAATAA
2801 TGTGATATCT TGTTGTAAAA TTTAATTACA TCTAATATAA CGGTGTGATT
2851 AGATTGTATG TTGGATAACA TGCCCATCGG TTGGCTTATT TAGGGAATAA
2901 GCCAAATGGT ATATTTGCAA ACGAAAAATA ATTTGTAAAT AAAACTTTTA
2951 TGTATGTATT CTTAACGATC TAGCAGCAAA GGCTGAAAAA TAAACTTCGA
3001 TGAAAAATCT CAAAATCAAC TCTTAAAAAT TAAATTTTGG CTTATAAGTA
3051 TAGTTCCTAA CTAGTTTAGA AGAAAAAATA TTTAAAGCGG GGAAGAGGAA
3101 AAGGAATAAA CTAATAGCTA AATTATTGCA TGCATGTAGC GATTTGAGGA
3151 CGACCGAGTT GTTTTGTCTG GATCAGCCGA CCGAGACAGA GCAATCTTCT
3201 TTAATCATAA ATAACCAGAA AAACCATACC AGTTCATCAC AATGGACCGA
3251 GTCAGAGTCA TTACATATTT TTCATTGTTG CGCACAGGAT TCACCATGTT
3301 CTTATGGGAA ATATTTTTAA CTCTCAAATG GTTATGATTT TGAACCTCTA
3351 TTTTGTAGAG AGAATTAACA AGCGAGCGAG CAATCAGGCC AAAAAGGGAG
3401 AAAGAAAATT ATTTTGTGTA ATTTTTFMTT AAGGTAGGGT GGAGGAGTCA
3451 TTACATGATT TTTTTTTATA TTCCCTCGTT GATTATATGC TGTTCAAATG
3501 GTTATGATTT TTTTAAAAGA TAACAACAAT ACAAATTAGT ATGTGATAGA
3551 TCATTTTCAG AGCATATAGG ATTAAATTTA ACTTCTGTAA ATTACAAAAC
3601 AAACAAGTTT AACTGTTAAT ATACATTAAA TTTGTTTTTT TCAACTTAGG
3651 AATTGAATTT TATGTATATA TTTGTAAAAT GATATATTAA TTTATTTTTT
3701 TAAAAAATA ATTATTTAGA TAACACGCAA ACTAGAAAAC CACCGCAGAA
3751 GTTCTCATAT TTCTTGTCTT ATCTGCACTT GCAGAGCTGA TGCTGCTGGG
3801 CTTCATATCC CTGCTTCTCA CCGTGGCACA GGCGCCCATC TCCAAGATCT

FIGURE 8 cont'd

3851 GCATCCCCAA GTCGGCTGCC AACATCTTGT TGCCGTGCAA GGCAGGCCAA
3901 GATGCCATCG AAGAAAGAAG CAGCAAGTGG TCGCCGGTCC TTGGCCGGCG
3951 CCGGCGGCGG GGACTIONTGC TCGAAATTTC ATGTGAGAAT AACACCAGCT
4001 GCCGGCAAGC ACAACCTCGA TGCAATAACT AATTTAACTA TAATTGATTT
4051 TTCTTGGGTT TTCTGCAGGG CAAGGTGGCG CTGATGTCGG CAAAGAGCAT
4101 GCACCAGCTG CACATTTTCA TCTTCGTGCT CGCCGTGTTT CATGTTACCT
4151 ACTGCATCAT CACCATGGGT TTAGGGCGCC TCAAAGTGAG TTTGTCGTTC
4201 TGTCCCTCAT GCACATGTTT TCTCTAGTTC TAGCAAGATT GTCAGTCCTT
4251 CAAATGGATT GTTTCGACAA GAAACCCAAT TTATTAATTT GCCAGTAAAT
4301 ATATAATAAT TGATCTTTCT TGGTTTTAGA TGAAGAAATG GAAGAAGTGG
4351 GAGTCACAGA CCAACTCATT GGAGTATCAG TTCGCAATCG GTAGTGAATT
4401 AAGAATCTCC CTAACATTTT CATTTTCAGAA CCTTTATGAT AATGTCTTGA
4451 AAGAGGAGGA GCAAATCAGC TGAAAAATAT GATCGATCCA TGCAGATCCT
4501 TCACGATTCA GGTTTCACGA TCAGACGTCG TTCGTGAAGC GGCATCTGGG
4551 ATCATTTCTA AGCACCCCTG GGCTCAGATG GATCGTGAGT TATCAATCTC
4601 CGAATACATG CTTGTTTTTTT ATTCTTGCAA CTGGCCTAGC TGTTCCAATT
4651 CAATCCATAT TTTTTGAAAA AAAAAATATT CATGCCGTGT TTGTTGTTAG
4701 GTAGCATTTCT TCAGGCAGTT CTTTGGGTCC GTCACCAAGG TGGACTACCT
4751 GACCATGCGG CAAGGCTTCA TCAATGTATA TACTAATCAA ACCTGACCAA
4801 TTCAACATTG ATGATGCAAA CAGAGACCAG GTTTTTTTTTT TCGAGTGTGC
4851 ATTGAGTAAT GGTTTTAGCT TCTTCTCTTT TGCAGGCGCA TTTGTCGCAG
4901 AATAGCAAGT TCGACTTCCA CAAATACATC AAGAGGTCTT TGGAGGACGA
4951 CTTCAAAGTT GTCGTTGGCA TCAGGTCCGT CCTCGCTTTA TTAATTATAG
5001 GACTCTTATA TTCAACATTT TTTTATAAAA GAAACATATT TAGTCTCCAG
5051 TTGTGTATGT GTATGTGGAT CTTGACACAT TTGGCTGGTT TTGCAGCCTC
5101 CCTCTGTGGT TCGTCGGAAT CCTGTACTC TTCCTCGATA TCCACGGTAA
5151 TCCTTGTCCT ATTTCAATTCT TTTTTTTACT CTCAAACCT TGTTCTGAAT
5201 TGGTCTTATA ATCACCATCG ATTTTTTTTC AACTTTTTTC CCGCGTGTAG
5251 GTCTTGGCAC ACTTATTTGG ATCTCTTTTG TTCCTCTCAT CGTAAGAGCG
5301 AAATTTCCCT GTCCAAAGAA ACAGTTAACA TAATTAATTA TGCTTTAATT
5351 TATCATGAAA ATTAATATGA TCATATAACT AATGAACAAA CATTATGTGT
5401 AATGCCACCG TTGTCTCAGA TCGTCTTGT AGTTGGGACC AAGCTAGAGA
5451 TGGTGATCAT GGAGATGGCC CAAGAGATAC AGGACAGGGC CACTGTGATC
5501 CAGGGAGCAC CTATGGTTGA ACCAAGCAAC AAGTACTTCT GGTTCACCG
5551 CCCTGACTGG GTCTTGTCTT TCATACACCT GACACTCTTC CATGTACATG
5601 TTTAAAACCT AAACCTTGCT GCTCAACTAC AAATAGTACT TTATCTTTCA
5651 CAATTAACAC CTAATTAAC AACTAGCAT CCATCCATTT GTGGCTACTG
5701 ATCGATGGGA CGACGGATCG ATCATCACCA GAACGCATTT CAGATGGCGC
5751 ATTTCTGTATG GACTATGGTG TGTATGCTAC TTGCTTAGTT GTTGCCATTA

Figure 8 cont'd

5801 TCAGTTCCTTA AGCAAATTAA GTGTGATGCA TGCCTGACT AATGAGACAA
 5851 AAAATGACAC AGCTTGTTCA TCGATCTGGT TGTMTTGTGT GTGACAGGCA
 5901 ACACCTGGTC TGAAGAAATG CTTCCATGAA AATATTTGGC TGAGCATCGT
 5951 GGAAGTCATT GTGGGGATCT CTCTTCAGGT GCTATGCAGC TACATCACCT
 6001 TCCCGCTCTA CGCGCTCGTC ACACAGGTGA ACAAGCCATT CACAAATTCCT
 6051 ATTAGCCGTT TCTTAATTGA TGACACTGTT AATTTTATGA CACACGTTTT
 6101 GACCATTTGT CTTATTAAAA ATATTTATGT AATTATCATT TGAGTTGTTT
 6151 TATCACTAAA AGTACTTTTT AAATAATTTA TATTTTGCAT TTGTACAATT
 6201 CTTTTAATAA GATAATGGTC AAACATGTGT CCAAAAGTTA ACAGCATCAT
 6251 CTATTAAGAA AAGGAGGGGT TTTTTTTTTT TGGAATTTTG CAAAATTTGT
 6301 TCAAAATCAG TCCAAAACCT TTTTTTTTTT CGAAATTTCA GTTTCCTAC
 6351 CAGTCCCAT AAAATGTCTT TTCTTTATTT CCACAAGATT GAACCCATGA
 6401 GATGCCCTTT GTGTTGGTAT GTGTTTTGGC CATCACTTGC AGATGGGATC
 6451 GAACATGAAG AAGACAATTT TCGAGGAGCA AACGATGAAG GCGCTGATGA
 6501 ACTGGAGGAA GAAAGGCGATG GAGAAGAAGA AGGTCCGGGA CGCCGACGCG
 6551 TTCCTGGCGC AGATGAGCGT CGACTTCGCG ACGCCGGCGT CGAGCCGGTC
 6601 CGCGTCGCGG GTGCACCTGC TGCAGGTCAC AGGGCGGGTC GGACGCCCCG
 6651 CGAGCCCAAT CACGCTGGCC TCACCACCGG CACCGGAGGG GACATGTACC
 6701 CGGTGCCCGG CGCGGCTCGG TCTCGCCAGC TGCTAGACGA CCCGCCGGAC
 6751 AGGAGGTGGA TGGCATCCTC GTCGGCCGAC ATCGCCGATT CTGATTTTTC
 6801 CTTCAGCGCA CAACCGTGAC GGGGGCGATC GGTTCCTGTA TTGATGCTGT
 6851 ACCAAACATA GGAGTTTAAT ATATATATAA TTGTTACGGT AAAATCTAAT
 6901 TATTGTGCGC GCACTTATAT TAGTCTTATA GCGCGACTGG TTCGTGATTA
 6951 GACAAGGTGA TGCATGCTGT TTAGTTATAA AGGATATCAG CGCAGCTAAA
 7001 AAAACTTACT CCCTACTTAA TAGATGACCT CGTTGATTTT TAACATTATT
 7051 CGTCTTATTT AAAAAATTTA TGCAAATGTT TAAACATAA ATCATGCTTA
 7101 AAGTACTTTT AGTGATAAAA CAACCTTACAA CAAAATAAAT TATAGTTACC
 7151 TAATTTTTTT TAATAAATCG AATGG

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1 TTATACCATG TGAGAAAGGC TGGAAAGCATA TGCTCTTAGC AGGGACGCGT
51 GCATGTTTAT ATAGGAGGCA TAAGCCGAAG AGATATACAT GAGGAGAGGT
101 TTAAGATCAG TCTATCTTAT TTACAGTTTA AACACAAGGA GATAGAAAGA
151 GATCCTAACC TACACATGTT ATACAAGTCA CGTATAATAC AAGAGTTATT
201 TCGTCTAACA CCTTCCCCTC TGATATGATA AGTCGCCGGG AGAGAGAGAG
251 AGTGTGTGGC TGCCCTCGCT GCACTGCACG CACATGTTTA CTTCTCCGAC
301 TGAAACCACG GTGAAACCGG CGGCGGTGTC GCACTCCCCT GACTTTCCTC
351 GCCGGGGTCC CGTCCGGACA ATTAAACCGT CTGTACCTGC CGGGCGTCTGA
401 CCCGATCGTG ATGTGGCGCC GCTTTGTCTG CAGCGAGCTG CGTGGCCGAT
451 GGCAACAAAA CTGCGGTCAC ATACATGCAT ACCCCGCATA CCCCGACGCT
501 CACCAGTAAG TAGGCTGTGG TGCGGCACCA CGGGCTCGCC GCCATTTCATG
551 CCATGCATGG GCCACCCGCC GCGGAAACCG CCGCGCTGCT GCCTGCCACC
601 CCGCCGCCGT TGACGAAGAC TTCGCCC GGC CATCCATAAA AGCATGCATG
651 GCTTGCTCTC ACCGGTCCGG CCACACACAC CACACTTCAC TTCGCCATTC
701 GCACCACCGA GAGCGTAGCG TAACGTGTGT TTGAAGTCCT ACCATTAATT
751 TTGCTGGATC GATGGCTGGG CCGGCGGGAG GTCGGGAGCT GTCGGACACG
801 CCGACGTGGG CGGTGGCGGT AGTCTGCGCC GTCATGATAC TCGTCTCCGT
851 CGCCATGGAG CACGCGCTCC ACAAGCTCGG CCACGTACGT GCTCTCGGTT
901 CACTAGTGCT TAACTGTTTT TGATGTTTTT GGGCGTGTTT GG TAGCCTGC
951 ATGGAGAGTG TATGAGCCCA AAAGTTCCTT CCCCAGCCCA CTTTTCGCTG
1001 TTTGGTAGGG TGTATGGGCT GAGGAGAGCA TGCATCAACT GATGCAAAAA
1051 GGGCCTCAGC ATAGCTGAGC CCAGCACCCC CGCAGAGGCG AGCTGAGGCG
1101 AGTTATGCTG AGCCCATGCA CCTTCGCCCC GTCGCCCCGT CGCCCCGTGC
1151 CTCCCCCCTT GCACCTCTTC CTCCTCCCTC TTCCTACCAA ACACAGTCTC
1201 ATCCAAACAT GTAACAACAC ATGCATGACC ACCAAACAAC TGAAGATGAA
1251 TGTATTCATC ATGTCTATAC TTACCATGCA TCAACAGGGA ACAACTATGC
1301 TAGGGTGAGA ACAGCTGCCA AACACACCCG TGCACCTACT CATGCTGTGC
1351 CGGCGCTGGC GTACGTGTGC AGTGGTTCCA CAAGTGGCGC AAGAAGGCCG
1401 TGGGGGAGGC GCTGGAGAAG ATGAAGGCGG AGCTCATGCT GGTGGGCTTC
1451 ATATCCCTGC TCCTCATCGT CACGCAGGAT CCCGTCTCCA GGATCTGCAT
1501 CTCCAAGGAG GCCGGCGAGA AGATGCTCCC GTGCAAGCCT TACGACGGCG
1551 CCGGCGGTGG CAAAGGCAAG GACAATCACC GGAGGCTTCT CTGGCTCCAA
1601 GGCGAGAGCG AGACCCACCG CCGGTTCTTG GCTGCCCCCG CCGGAGTGGA
1651 CGTCTGCGCC AAACAGGTGA GCACCTAGCG TCGCCACAAA CCACAAACTA
1701 GCTAATGAGC ATGGACCTGA ATTTCTTCTC TTCTTGGCTT GGCTTGACTA
1751 AATTGGTTGT GCAGGGCAAG GTGGCGCTGA TGTCAGCGGG AAGCATGCAC
1801 CAACTGCACA TATTCATCTT CGTGCTCGCC GTCTTCCACG TCTTGACAG
1851 CGTCGTCACC ATGACCCTAA GCCGTCTCAA AGTGAGCATC ATACTCGAGC

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1901 TGTTTGTCAA TAATCCTTGG TTTCCAATCC AATTCCAAAG CTGGCACTGA
1951 TCCTGCTCCG GCTTCTTGCA GATGAAGCAA TGGAAGAAGT GGGAGTCGGA
2001 GACCGCCTCG CTGGAGTATC AGTTCGCGAA TGGTCAGCTT CAACTTTTCT
2051 TACTGAAACC GGATGCATTT ACAACAAACG CACGCACGAT CAATCATCAC
2101 AGTGTGAGCC GATACGTTGA ACCGATTGAA TCCTCGCAGA TCCATCGCGG
2151 TGCCGGTTCA CGCACCAGAC GACGTTGGTG AGGCGGCACC TGGGCCTCTC
2201 CAGCACCCCC GGCCTCAGAT GGGTGGTGGC CTTCTTCAGG CAGTTCTTCA
2251 CGTCGGTGAC CAAGGTGGAC TACCTGACCT TGCGGCAGGG CTTTCATCAAC
2301 GCGCATCTCT CGCAGGGCAA CAGGTTTCGAC TTCCACAAGT ACATCAAGAG
2351 GTCGTTGGAG GACGACTTCA AAGTCGTCGT CCGCATCAGG TACGCGCCAT
2401 TCCTTTCTCT GCACAAATTA ATACATCCAC CACCACATAG GTAGATAGAT
2451 AGATCGATAG ATAGATTATA CAAGTGCCGG TACGTACGTA CGTCTCATAT
2501 GATCTTGACA CATCTGTCCT CTTGCCGCAG TCTCAAGCTC TGGTTCGTGG
2551 CGGTCCTCAT CCTCTTCCTT GATTTTCGACG GTAGCCGCCT TGTCCATGCC
2601 CTGCTCGCCC TCTCCTCCGC TTCTCTCCAT AATTTGTGAA CTTGTCCCGT
2651 ATATAACCAC ACCACCGTCG TCTTCTCGCA GGGATCGGCA CTCTTCTCTG
2701 GATGTCCGTG GTTCCTCTCG TGGTAAGTCC ACAATTTGAA TAGACAACCT
2751 GTCCAATTGT GATGTACAGT ACCTCCAAAC TTAATTAACA TGTCAATTGC
2801 TGATGTCTTG CGTGTAACAT TAGATCCTCT TGTGGGTGG GACCAAGCTG
2851 GAGATGGTGA TCATGGAGAT GGCCCAGGAG ATCCATGACC GGGAGAGCGT
2901 CGTCAAGGGT GCTCCCGCCG TCGAGCCCAG CAACAAGTAC TTCTGGTTCA
2951 ACCGGCCTGA CTGGGTCTCT TTCTCATGC ACCTCACACT CTTCCAGAAC
3001 GCGTTTCAGA TGGCTCATTT CGTGTGGACA GTGGTACGTA CAAGTACTTG
3051 TCACTTCACT TAGGCTAACT CCAACAAACG ACCCCAAATT AATGGTCCGT
3101 CGCGTCTGTT TGGGGTATGT TTGGGGTAAA CGGACACAAA ACTCAATCCA
3151 ACGCGCGGTA GCAAACGAAC GTTTTTCGGT ACGTTTTCGT CCGCTTTCGC
3201 CCCATCCCAG CCCAAATTCG TTGACGTTGT TGCATCGCAG GCCACGCCCC
3251 GCTTGAAGAA ATGCTACCAC GAGAAAATGG CAATGAGCAT CGCCAAGGTC
3301 GTGCTGGGGG TAGCCGCCCA GATCTTGTGC AGCTACATCA CCTTCCCGCT
3351 CTACGCGCTC GTCACGCAGA TGGGCTCACA CATGAAGAGA AGCATCTTCG
3401 ACGAGCAGAC GGCCAAGGCG CTGACCAACT GCGGAAAGAT GGCCAAGGAG
3451 AAGAAGAAGG CCCGAGACGC GGCCATGCTG ATGGCGCAGA TGGGCGGCGG
3501 CGCGACGCCG AGCGTCGGCT CGTCGCCGGT GCACCTGCTC CACAAGGCCG
3551 GGGCGCGGTC CGACGACCCC CAGAGCGTGC CGGCGTCCCC GAGGGCCGAG
3601 AAGGAAGGCG GCGGCGTGCA GCATCCGGCG CGCAAGGTAC CTCCTTGTGA
3651 CGGGTGGAGG TCGGCCTCGT CGCCGGCGCT CGACGCTCAC ATCCCCGGTG
3701 CAGATTTTGG CTTCAGCACG CAACGTTGAC CGATCAGACA AGTTCCTTTT
3751 TTTTTCGGTG AATAGAAGCG TATCATTTCA TTGATAGACA GTAGAAATTA
3801 CAGGAATGGC TGTCTACTA CTATGTACAC AAGGGCACAG CAAAGGATCA

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Figure 9 cont'd

3851 TTGATCTTGT TACAAGAGCA GTAGAAAGGG ATTGCTCTCC ATTGATCTTG
3901 TTAAGTTGTA TETCACAAAT TGTTCAGAA AAAAGTGTAT GTCATCCCAA
3951 CCAAGAGCTG AGTTTGTGAT GATTCGTGCA ATAAGAATTG CAAGTTTCAC
4001 CGAGTCAAAA ATGAAGCTTC TAAGTACGCA CCAACCAACG GACTCTTTCA
4051 TCTCAACAAA AGAACTGTAA ATGGCAATAA TTCTGATAAC ATCGGAAGGG
4101 AGCTC

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Figure 10

1 ATGGCAGGTG GGAGATCGGG ATCGCGGGAG TTGCCGGAGA CGCCGACGTG
 51 GCGGGTGGCC GTCGTCTGCG CCGTCCTCGT GCTCGTCTCC GCCGCCATGG
 101 AGCAGGGCCT CCACAACCTC AGCCATAAAA CCACCGCAGA AGTTCTCATA
 151 TTTCTTGTCC TATCTCCACT TGCAGAGCTG ATGCTGCTGG GCTTCATATC
 201 CCTGCTTCTC ACCGTGGCAC AGGCGCCCAT CTCCAAGATC TGCATCCCCA
 251 AGTCGGCTGC CAACATCTTG TTGCCGTGCA AGGCAGGCCA AGATGCCATC
 301 GAAGAAGAAG CAGCAAGTGG TCGCCGGTCC TTGGCCGGCG CCGGCGGGCG
 351 GGACTACTGC TCGAAATTCTG ATGGCAAGGT GCGCTGATG TCGGCAAAGA
 401 GCATGCACCA GCTGCACATT TTCATCTTCG TGCTCGCCGT GTTCCATGTT
 451 ACCTACTGCA TCATCACCAT GGGTTTAGGG CGCCTCAAAA TGAAGAAATG
 501 GAAGAAGTGG CAGTCACAGA CCAACTCATT GGAGTATCAG TTCGCAATCG
 551 ATCCTTCACG ATTCAGGTTC ACGCATCAGA CGTCGTTCGT GAAGCGGCAT
 601 CTGGGATCAT TCTCAAGCAC CCCTGGGCTC AGATGGATCG TAGCATTCTT
 651 CAGGCAGTTC TTTGGGTCCG TCACCAAGGT GGACTACCTG ACCATGCGGC
 701 AAGGCTTCAT CAATGCGCAT TTGTCGAGA ATAGCAAGTT CGACTTCCAC
 751 AAATACATCA AGAGGTCTTT GGAGGACGAC TTCAAAGTTG TCGTTGGCAT
 801 CAGCCTCCCT CTGTGGTTCG TCGGAATCCT TGTACTCTTC CTCGATATCC
 851 ACGGTCTTGG CACACTTATT TGGATCTCTT TTGTTCTCTC CATCATCGTC
 901 TTGTTAGTTG GGACCAAGCT AGAGATGGTG ATCATGGAGA TGGCCCAAGA
 951 GATACAGGAC AGGGCCACTG TGATCCAGGG AGCACCTATG GTTGAACCAA
 1001 GCAACAAGTA CTTCTGGTTC AACCGCCCTG ACTGGGTCTT GTTTTTCATA
 1051 CACCTGACAC TCTTCCATAA CGCATTTTCA AGTGGCGCATT TCGTATGGAC
 1101 TATGGCAACA CCTGGTCTGA AGAAATGCTT CCATGAAAT ATTTGGCTGA
 1151 GCAATCGTGA AGTCATTGTG GGGATCTCTC TTCAGGTGCT ATGCAGCTAC
 1201 ATCACCTTCC CGCTCTACGC GCTCGTCACA CAGATGGGAT CGAACATGAA
 1251 GAAGACAATT TTCGAGGAGC AACCGATGAA GGCGCTGATG AACTGGAGGA
 1301 AGAAGGCGAT GGAGAAGAAG AAGGTCCGGG ACGCCGACGC GTTCCTGGCG
 1351 CAGATGAGCG TCGACTTCGC GACGCCGGCG TCGAGCCGGT CCGCGTCGCC
 1401 GGTGCACCTG CTGCAGGTCA CAGGGCGGGT CGGACGCCCC CCGAGCCCAA
 1451 TCACGGTGGC CTCACCACCG GCACCGGAGG AGGACATGTA CCCGGTGCCG
 1501 GCGGCGGGCTG CGTCTCGCCA GCTGCTAGAC GACCCGCCGG ACAGGAGGTG
 1551 GATGGCATCC TCGTCGGCCG ACATCGCCGA TTCTGATTTT TCCTTCAGCG
 1601 CACAACGGTG A

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Figure 11

1 ATGGCTGGGC CGGCGGGAGG TCGGGAGCTG TCGGACACGC CGACGTGGGC
 51 GGTGGCGGTA GTCTGCCCGG TCATGATACT CGTCTCCGTC GCCATGGAGC
 101 ACGCGCTCCA CAAGCTCGGC CACTGGTTCC ACAAGTGGCG CAAGAAGGCC
 151 CTGGGGGAGG CCCTGGAGAA GATGAAGGCG GAGCTCATGC TGGTGGGCTT
 201 CATATCCCTG CTCTCATCG TCACGCAGGA TCCCGTCTCC AGGATCTGCA
 251 TCTCCAAGGA GGCCGGCGAG AAGATGCTCC CGTGCAAGCC TTACGACGGC
 301 GCCGGCGGTG GCAAAGGCAA GGACAATCAC CGGAGGCTTC TCTGGCTCCA
 351 AGCGGAGAGC GAGACCCACC GCCCGTTCCT GGCTGCCCCG GCCGGAGTGG
 401 ACGTCTGCEC CAAACAGGGC AAGGTGGCGC TGATGTCAGC GCGAAGCATG
 451 CACCAACTGC ACATATTCAT CTTCGTGCTC GCCGTCTTCC ACGTCTTGTA
 501 CAGCGTCGTC ACCATGACCC TAAGCCGTCT CAAAATGAAG CAATGGAAGA
 551 AGTGGGAGTC GGAGACCGCC TCGCTGAGT ATCAGTTCCG GAATGATCCA
 601 TCGCGGTGCC GGTTCACGCA CCAGACGACG TTGGTGAGGC GGCACCTGGG
 651 CCTCTCCAGC ACCCCCGGCG TCAGATGGGT GGTGGCCTTC TTCAGGCAGT
 701 TCTTCACGTC GGTGACCAAG GTGGA CTACC TGACCTTGGC GCAGGGCTTC
 751 ATCAACGCGC ATCTCTCGCA GGGCAACAGG TTCGACTTCC ACAAGTACAT
 801 CAAGAGGTCG TTGGAGGACG ACTTCAAAGT CGTCGTCCGC ATCAGTCTCA
 851 AGCTCTGGTT CGTGGCGGTC CTCATCCTCT TCCTTGATTT CGACGGGATC
 901 GGCACTCTTC TCTGGATGTC CGTGGTTCCT CTCGTGATCC TCTTGTTGGT
 951 TGGGACCAAG CTGGAGATGG TGATCATGGA GATGGCCCAG GAGATCCATG
 1001 ACCGGGAGAG CGTCGTCAAG GGTGCTCCCG CCGTCGAGCC CAGCAACAAG
 1051 TACTTCTGGT TCAACCGGCC TGA CTGGGTCTCTTCTCA TGCACCTCAC
 1101 ACTCTTCCAG AACGCGTTTC AGATGGCTCA TTTCGTGTGG ACAGTGCCCA
 1151 CGCCCGGCTT GAAGAAATGC TACCACGAGA AAATGGCAAT GAGCATCCCC
 1201 AAGGTCTGTC TGGGGGTAGC CGCCAGATC TTGTGCAGCT ACATCACCTT
 1251 CCCGCTCTAC GCGCTCGTCA CGCAGATGGG CTCACACATC AAGAGAAGCA
 1301 TCTTCGACGA GCAGACGGCC AAGGCGCTGA CCAACTGGCG AAAGATGGCC
 1351 AAGGAGAAGA AGAAGGCCCC AGACGCGGCC ATGCTGATGG CGCAGATGGG
 1401 CGGCGGCGCG ACGCCGAGCG TCGGCTCGTC GCCGCTGCAC CTGCTCCACA
 1451 AGGC CGGGG GCGCTCCGAC GACCCCAAGA GCGTGCCGGC GTCCCCGAGG
 1501 GCGGAGAAGG AAGGCGGCGG CGTGCAAGAT CCGGCGCCCA AGGTACCTCC
 1551 TTGTGACGGG TGGAGGTGCG CCTCGTCGCC GCGGCTCGAC GCTCACATCC
 1601 CCGCTGCAGA TTTTGGCTTC AGCACGCAAC GTTCGA

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1	GTTGGTACAT	AAAAGACTCT	TCCTTTGTCT	GTTTTTTGTT	CCCAGATTCA
51	TCTTTACTTA	TTGACTAAAT	TCTCTCTGGT	GTGAGAAGTA	AAATGGGTCA
101	CGGAGGAGAA	GGGATGTCGC	TTGAATTCAC	TCCGACGTGG	GTCGTCGCCC
151	GAGTTTGTA	GGTCATCGTC	GCGATTTTCA	TGGCGGTGGA	GCGTTTGCTT
201	CACTATTTTC	GTACTGTTCT	TAAGAAGAAG	AAGCAAAAAC	CCCTTTACGA
251	AGCCCTTCAA	AAGGTTAAAG	AAGAGCTGAT	GTTGTTAGGG	TTTATATCGC
301	TGTTACTGAC	GGTATTCCAA	GGGCTCATTT	CCAAATTTCT	TGTGAAAGAA
351	AATGTGCTTA	TGCATATGCT	TCCATGTTCT	CTCGATTCAA	GACGAGAAGC
401	TGGGGCAAGT	GAACATAAAA	ACGTTACAGC	AAAAGAACAT	TTTCAGACTT
451	TTTTACCTAT	TGTTGGAACC	ACTAGGCGTC	TACTTGCTGA	ACATGCTGCT
501	GTGCAAGTTG	GTTACTGTAG	CGAAAAGGGT	AAAGTACCAT	TGCTTTTCGT
551	TGAGGCATTG	CACCATCTAC	ATATTTTCAT	CTTCGTCCTC	GCCATATCCC
601	ATGTGACATT	CTGTGTCCTT	ACCGTGATTT	TTGGAAGCAC	AAGGATTCAC
651	CAATGGAAGA	AATGGGAGGA	TTGATCGCA	GATGAGAAGT	TTGACCCCGA
701	AACAGCTCTC	AGGAAAAGAA	GGGTCACTCA	TGTACACAAC	CATGCTTTTA
751	TTAAAGAGCA	TTTTCTTGGT	ATTGGCAAAG	ATTCAGTCAT	CCTCGGATGG
801	ACGCAATCCT	TTCTCAAGCA	ATTCTATGAT	TCTGTGACGA	AATCAGATTA
851	CGTGACTTTA	CGTCTTGGTT	TCATTATGAC	ACATTGTAAG	GGAAACCCCA
901	AGCTTAATTT	CCACAAGTAT	ATGATGCGCG	CTCTAGAGGA	TGATTTCAAA
951	CAAGTTGTTG	GTATTAGTTG	GTATCTTTGG	ATCTTTGTCT	TCATCTTTTT
1001	GCTGCTAAAT	GTTAACGGAT	GGCACACATA	TTTCTGGATA	GCATTTATTC
1051	CCTTTGCTTT	GCTTCTTGCT	GTGGGAACAA	AGTTGGAGCA	TGTGATTGCA
1101	CAGTTAGCTC	ATGAAGTTGC	AGAGAAACAT	GTAGCCATTG	AAGGAGACTT
1151	AGTGGTGAAA	CCCTCAGATG	AGCATTTCTG	GTTTCAGCAA	CCTCAAATTG
1201	TTCTCTACTT	GATCCATTTT	ATCCTCTTCC	AGAATGCTTT	TGAGATTGCG
1251	TTTTTCTTTT	GGATTTGGGT	TACATACGGC	TTGACTCGT	GCATTTATGG
1301	ACAGGTGAGA	TACATTGTTT	CAAGATTGGT	TATCGGGGTC	TTTATTCAAG
1351	TGCTTTGCAG	TTACAGTACA	CTGCCTCTTT	ACGCCATCGT	CTCACAGATG
1401	GGAAGTAGCT	TCAAGAAAGC	TATATTTCAG	GAGAATGTGC	AGGTTGGTCT
1451	TGTTNGTTGG	GCACAGAAAG	TGAAACAAAA	GAGAGACCTA	AAAGCTGCAG
1501	CTAGTAATGG	AGACGAAGGA	AGCTCTCAGG	CTGGTCCTGG	TCCTGATTCT
1551	GGTTCTGGTT	CTGCTCCTGC	TGCTGGTCCCT	GGTGCAGGTT	TTGCAGGAAT
1601	TCAGCTCAGC	AGAGTAACAA	GAAACAACGC	AGGGGACACA	AACAATGAGA
1651	TTACACCTGA	TCATAACAAC	TGAGCAGAGA	TATTATCTTT	TCCATTTAGA
1701	GGATCATCAT	CAGATTTTAG	CTTCAAGGTC	CGGTTTTGTG	GTTTATACAT
1751	AAGTTATAGT	GACTTGATTT	TTTTGTTTTG	TTACAAAGTT	ACCATCTTTG
1801	GATTAGAATT	GGGAAATTGA	ATCTGTTTGT	ATATTGTATT	ATTTGGAACA
1851	TTGTGGATGC	CCATGGATAT	GTTTCTGTTC		

1 MAGGRSGSRE LPETPTWAVA VVCAVLVLVS AAMEHGLHNL SHKTTAEVLI
51 FLVLSALAE LMLGFISLLL TVAQAPISKI CIPKSAANIL LPCKAGQDAI
101 EEEAASGRRS LAGAGGGDYC SKFDGKVALM SAKSMHQLHI FIFVLAVFHV
151 TYCIITMGLG RLKMKKKKKW ESQTNSLEYQ FAIDPSRFRF THQTSFVKRH
201 LGSFSSTPGL RWIVAFFRQF FGSVTKVDYL TMRQGFINAH LSQNSKFDFH
251 KYIKRSLEDD FKVVVGISLP LWFVGILVLF LDIHGLGTLI WISFVPLIIV
301 LLVGTKLEMV IMEMAQEIQD RATVIQGAPM VEPSNKYFWF NRPDWWLFFI
351 HLTLFHNAFQ MAHFVWTMAT PGLKKCFHEN IWLSIVEVIV GISLQVLC SY
401 ITFPLYALVT QMGSNMKTII FEEQTMKALM NWRKKAMEKK KVRDADAFLA
451 QMSVDFATPA SSRSASPVHL LQVTGRVGRP PSPITVASPP APEEDMYPVP
501 AAAASRQLLD DPPDRRWMA'S SSADIADSDF SPSAQR*

1 MAGPAGGREL SDTPTWAVAV VCAVMILVSV AMEHALHKLG HWFHKWRKKA
51 LGEALEKMKA ELMLVGFISL LLIVTQDPVS RICISKEAGE KMLPCKPYDG
101 AGGGKGDNDH RRLWLQGES ETHRRFLAAP AGVDVCAKQG KVALMSAGSM
151 HQLHIFIFVL AVFHVLYSVV TMTLSRLKMK QWKKWESETA SLEYQFANDP
201 SRCRFTHQTT LVRRHLGLSS TPGVRWVVAE FRQFFTSVTK VDYLTLRQGF
251 INAHLSQGNR FDFHKYIKRS LEDDFKVVRV ISLKLWVAV LILFLDFDGI
301 GTLLWMSVVP LVILLWVGTK LEMVIMEMAQ EIHDRSEVVK GAPAVEPSNK
351 YFWFNRPDWW LFLMHLTLFQ NAFQMAHFVW TVATPGLKKC YHEKMAMSIA
401 KVVLGVAQAI LCSYITFPLY ALVTQMGSIM KRSIFDEQTA KALTNWRKMA
451 KEKKKARDAA MLMAQMGGA TPSVGSSPVH LLHKAGARSD DPQSVPASPR
501 AEKEGGGVQH PARKVPPCDG WRSASSPALD AHIPGADFGF STQR*

Figure 15

1 MGHGSGMSL EFTPTWVAG VCTVIVAISL AVERLLHYFG TVLKKKKOKP
51 LYEALQKVKE ELMLLGFISL LLTVFQGLIS KFCVKENVLM HMLPCSLDSR
101 REAGASEHKN VTAKERFQT? LPIVGTTRRL LAEHAQVVG YCSEKGVPL
151 LSLEALHHLH IFIFVLAISH VTFCVLTVIF GSTRIHQWKK WEDSLADEKF
201 DPETALRKRR VTHVHNHAFI KEHFLGIGKD SVILGWTQSF LKQFYDSVTK
251 SDYVTLRLGF IMTHCKGNPK LNFHKYMMRA LEDDFKQVVG ISWYLVIFVU
301 IFLLLVNGW HTYFWIAFIP FALLAVGTK LEHVIAQLAH EVAERHVAIF
351 GDLVVKPSDE HFWFSKPQIV LYLIHFILFQ NAFELAFFFW IWVTYGFDS
401 IMGQVRYIVP RLVICVFIQV LCSYSTLPLY AIVSQMGSSF KKAILEENVQ
451 VGLVGWAQKV KQKRDLCAAA SNGDEGSSQA GPGPDGSGS APAAGPGAGF
501 AGIQLSRVTR NNAGDTNNEI TPDHNN*

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FIGURE 16

[illegible]

FIGURE 16 (CONT/D)

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Hvml0-H1	AQILCSYITFF	PLYALVTQMG	SHMKRSIFDEE	QTSKALTNWR	KMAKEKKKAR	DAAMLMAQMI	
Mlo	LQFLCSYMTFF	PLYALVTQMG	SNMKRSIFDEE	QTSKALTNWR	NTAKEKKKVR	DTDMMLMAQMI	
Osmlo-H1m	LQVLCSYITFF	PLYALVTQMG	SNMKKKTIFEE	QTMKALMNNWR	KKAKEKKKVR	DADAFLAQMS	
Atmlo-H1	IQVLCSYSTFF	PLYALVTQMG	SNFKKKTIFEE	NVQVGLVGVWA	QKVQKKRDLK	AAASNGDEGS	
Consensus	-Q-LCSY-TF	PLYALVTQMG	S-MK--IF-E	QT-KAL-NWR	-AKEKKK-R	DA-- --AQM-	
Hvml0-H1	GGAATPSRGSS	PSVGS SPV	HLLHKKAGARS	DDPQSVPASP	RAEKEG	GGVQHPARK	
Mlo	GDA TP SRGSS	PMP SRGSSPV	HLLHKKGMGRS	DDPQSAPPTSP	RTQQEARDMY	PVVVAHPVHR	
Osmlo-H1m	VD...FAT	PASSRSPV	HLLQ.VTGRV	GRPPSPITVA	SPPAPEEDMY	PVPAAASRQ	
Atmlo-H1	SQA GPGPD SG	SGSAPAA GP.	...GAGFA	GIQLSRVTNRN	NAGDTNNEIT	PDPHNN*	
Consensus	-A-- --	-S-- --SPV	HLL-- --GR-	--P-S--T	-- --	P-- --	
Hvml0-H1	V...PPCDGWR	SASSPALDAH	IPGADDFGFST	Q R *			
Mlo	L...NPNDRRR	SASSSAL EAD	IPSADEFSESQ	G *			
Osmlo-H1m	LLDDPPDRRW	MASSS...AD	IADSDSESEBA	Q R *			
Atmlo-H1	...D-- --	...D-- --A-	...D-- --FS-	...			
Consensus	-E-D-- --	-ASS-- --A-	I-- --DF-FS-	...			